Phyre2

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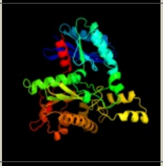
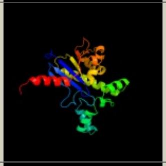
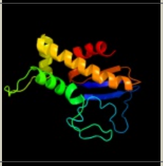
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x3nA_	Alignment		100.0	83	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of amppnp bound propionate kinase (tdcd) from2 salmonella typhimurium
2	c2iirJ_	Alignment		100.0	45	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
3	c1tuuA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase crystallized with atpgs
4	c3khyA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**propionate kinase; **PDBTitle:** crystal structure of a propionate kinase from francisella2 tularensis subsp. tularensis schu s4
5	c3p4iA_	Alignment		100.0	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetate kinase; **PDBTitle:** crystal structure of acetate kinase from mycobacterium avium
6	c1sazA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable butyrate kinase 2; **PDBTitle:** membership in the askha superfamily: enzymological2 properties and crystal structure of butyrate kinase 2 from3 thermotoga maritima
7	d2e1za2	Alignment		100.0	85	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
8	d1g99a2	Alignment		100.0	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
9	d2e1za1	Alignment		100.0	80	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
10	d1saza2	Alignment		100.0	26	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
11	d1g99a1	Alignment		100.0	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like

12	d1saza1	Alignment		100.0	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
13	c3eo3B_	Alignment		98.9	11	**PDB header:**isomerase, transferase **Chain:** B: **PDB Molecule:**bifunctional udp-n-acetylglucosamine 2-epimerase/n- **PDBTitle:** crystal structure of the n-acetylmannosamine kinase domain of human2 gne protein
14	d2aa4a2	Alignment		98.9	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
15	c2qm1D_	Alignment		98.8	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase from enterococcus faecalis
16	d2ap1a1	Alignment		98.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
17	d1z6ra3	Alignment		98.5	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
18	d2gupa2	Alignment		98.4	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
19	c1z6rC_	Alignment		98.4	14	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mlc protein; **PDBTitle:** crystal structure of mlc from escherichia coli
20	c2aa4B_	Alignment		98.4	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative n-acetylmannosamine kinase; **PDBTitle:** crystal structure of escherichia coli putative n-2 acetylmannosamine kinase, new york structural genomics3 consortium
21	d1z05a2	Alignment	not modelled	98.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
22	c1z05A_	Alignment	not modelled	98.2	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, rok family; **PDBTitle:** crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
23	c2ap1A_	Alignment	not modelled	98.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative regulator protein; **PDBTitle:** crystal structure of the putative regulatory protein
24	c2e2pA_	Alignment	not modelled	97.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hexokinase; **PDBTitle:** crystal structure of sulfolobus tokodaii hexokinase in2 complex with adp
25	c2gupA_	Alignment	not modelled	97.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rok family protein; **PDBTitle:** structural genomics, the crystal structure of a rok family protein2 from streptococcus pneumoniae tigr4 in complex with sucrose
26	c3r8eA_	Alignment	not modelled	97.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical sugar kinase; **PDBTitle:** crystal structure of a hypothetical sugar kinase (chu_1875) from2 cytophaga hutchinsonii atcc 33406 at 1.65 a resolution
27	c3vgkB_	Alignment	not modelled	97.8	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of a rok family glucokinase from streptomyces2 griseus
28	d2hoea2	Alignment	not modelled	97.7	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK

29	c3enoB_	Alignment	not modelled	97.6	18	**PDB header:**hydrolase/unknown function **Chain:** B: **PDB Molecule:**putative o-sialoglycoprotein endopeptidase; **PDBTitle:** crystal structure of pyrococcus furiosus pcc1 in complex2 with thermoplasma acidophilum kae1
30	c3mcpA_	Alignment	not modelled	97.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase; **PDBTitle:** crystal structure of glucokinase (bdi_1628) from parabacteroides2 distasonis atcc 8503 at 3.00 a resolution
31	d1q18a2	Alignment	not modelled	97.4	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
32	c2hoeA_	Alignment	not modelled	97.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetylglucosamine kinase; **PDBTitle:** crystal structure of n-acetylglucosamine kinase (tm1224) from2 thermotoga maritima at 2.46 a resolution
33	d1huxa_	Alignment	not modelled	97.3	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
34	d1sz2a1	Alignment	not modelled	97.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glucokinase
35	c1xc3A_	Alignment	not modelled	97.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructokinase; **PDBTitle:** structure of a putative fructokinase from bacillus subtilis
36	d2ewsa1	Alignment	not modelled	96.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
37	c3htvA_	Alignment	not modelled	96.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**d-allose kinase; **PDBTitle:** crystal structure of d-allose kinase (np_418508.1) from escherichia2 coli k12 at 1.95 a resolution
38	c2ch5D_	Alignment	not modelled	96.4	14	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nagk protein; **PDBTitle:** crystal structure of human n-acetylglucosamine kinase in2 complex with n-acetylglucosamine
39	d1xc3a2	Alignment	not modelled	96.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
40	c3gbtA_	Alignment	not modelled	95.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
41	c2q2rA_	Alignment	not modelled	95.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucokinase 1, putative; **PDBTitle:** trypanosoma cruzi glucokinase in complex with beta-d-glucose and adp
42	c3hz6A_	Alignment	not modelled	94.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
43	c3ifrB_	Alignment	not modelled	94.0	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
44	c2w40C_	Alignment	not modelled	93.7	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
45	c2ivoC_	Alignment	not modelled	93.1	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**up1; **PDBTitle:** structure of up1 protein
46	c1glbG_	Alignment	not modelled	92.6	17	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase
47	c2nlxA_	Alignment	not modelled	92.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
48	c3jvpA_	Alignment	not modelled	92.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
49	c1zc6A_	Alignment	not modelled	92.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable n-acetylglucosamine kinase; **PDBTitle:** crystal structure of putative n-acetylglucosamine kinase from2 chromobacterium violaceum. northeast structural genomics target3 cvr23.
50	c2d4wA_	Alignment	not modelled	91.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
51	d2i7pa1	Alignment	not modelled	91.4	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
52	c2cgkB_	Alignment	not modelled	90.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-rhamnulose kinase; **PDBTitle:** crystal structure of l-rhamnulose kinase from escherichia2 coli in an open uncomplexed conformation.
53	d2ch5a1	Alignment	not modelled	90.9	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
54	c3bf1C_	Alignment	not modelled	90.6	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**type iii pantothenate kinase; **PDBTitle:** type iii pantothenate kinase from thermotoga maritima2 complexed with pantothenate and adp

55	c2dpnB_	Alignment	not modelled	90.6	15	**PDB header:** transferase **Chain:** B: **PDB Molecule:** glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
56	c3ezwD_	Alignment	not modelled	90.5	17	**PDB header:** transferase **Chain:** D: **PDB Molecule:** glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
57	c3flcX_	Alignment	not modelled	90.5	18	**PDB header:** transferase **Chain:** X: **PDB Molecule:** glycerol kinase; **PDBTitle:** crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
58	d2p3ra1	Alignment	not modelled	90.4	17	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** Glycerol kinase
59	c3gg4B_	Alignment	not modelled	90.4	12	**PDB header:** transferase **Chain:** B: **PDB Molecule:** glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
60	c1zxoB_	Alignment	not modelled	90.3	15	**PDB header:** unknown function **Chain:** B: **PDB Molecule:** conserved hypothetical protein q8a1p1; **PDBTitle:** x-ray crystal structure of protein q8a1p1 from bacteroides2 thetaiotaomicron. northeast structural genomics consortium3 target btr25.
61	c3i8bA_	Alignment	not modelled	90.1	22	**PDB header:** transferase **Chain:** A: **PDB Molecule:** xylulose kinase; **PDBTitle:** the crystal structure of xylulose kinase from2 bifidobacterium adolescentis
62	c3g25B_	Alignment	not modelled	90.0	17	**PDB header:** transferase **Chain:** B: **PDB Molecule:** glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
63	c2zf5O_	Alignment	not modelled	89.8	18	**PDB header:** transferase **Chain:** O: **PDB Molecule:** glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
64	c1woqB_	Alignment	not modelled	87.9	18	**PDB header:** transferase **Chain:** B: **PDB Molecule:** inorganic polyphosphate/atp-glucomannokinase; **PDBTitle:** crystal structure of inorganic polyphosphate/atp-glucomannokinase from2 arthrobacter sp. strain km at 1.8 a resolution
65	d2f9wa2	Alignment	not modelled	86.5	31	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** CoaX-like
66	c2ychA_	Alignment	not modelled	86.1	11	**PDB header:** cell cycle **Chain:** A: **PDB Molecule:** competence protein pilm; **PDBTitle:** pilm-piln type iv pilus biogenesis complex
67	c3h6eB_	Alignment	not modelled	86.0	18	**PDB header:** transferase **Chain:** B: **PDB Molecule:** carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of a carbohydrate kinase from novosphingobium2 aromaticivorans
68	d3bexa1	Alignment	not modelled	84.8	15	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** CoaX-like
69	c3hi0B_	Alignment	not modelled	82.6	18	**PDB header:** hydrolase **Chain:** B: **PDB Molecule:** putative exopolyphosphatase; **PDBTitle:** crystal structure of putative exopolyphosphatase (17739545) from2 agrobacterium tumefaciens str. c58 (dupont) at 2.30 a resolution
70	d1r59o2	Alignment	not modelled	82.6	10	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** Glycerol kinase
71	c3lm2B_	Alignment	not modelled	82.3	15	**PDB header:** transferase **Chain:** B: **PDB Molecule:** putative kinase; **PDBTitle:** crystal structure of putative kinase. (17743352) from agrobacterium2 tumefaciens str. c58 (dupont) at 1.70 a resolution
72	c2c5sA_	Alignment	not modelled	81.0	22	**PDB header:** rna-binding protein **Chain:** A: **PDB Molecule:** probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
73	c3h1qB_	Alignment	not modelled	80.7	19	**PDB header:** structural protein **Chain:** B: **PDB Molecule:** ethanolamine utilization protein eutj; **PDBTitle:** crystal structure of ethanolamine utilization protein eutj from2 carboxydothermus hydrogenoformans
74	c2h3gX_	Alignment	not modelled	80.5	11	**PDB header:** biosynthetic protein **Chain:** X: **PDB Molecule:** biosynthetic protein; **PDBTitle:** structure of the type iii pantothenate kinase (coax) from bacillus2 anthracis
75	c3djcA_	Alignment	not modelled	78.6	26	**PDB header:** transferase **Chain:** A: **PDB Molecule:** type iii pantothenate kinase; **PDBTitle:** crystal structure of pantothenate kinase from legionella pneumophila
76	c1zbsA_	Alignment	not modelled	77.8	16	**PDB header:** structural genomics, unknown function **Chain:** A: **PDB Molecule:** hypothetical protein pg1100; **PDBTitle:** crystal structure of the putative n-acetylglucosamine kinase (pg1100)2 from porphyromonas gingivalis, northeast structural genomics target3 pgr18
77	d1t6ca1	Alignment	not modelled	76.9	14	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** Ppx/GppA phosphatase
78	d2i7na2	Alignment	not modelled	76.8	19	**Fold:** Ribonuclease H-like motif **Superfamily:** Actin-like ATPase domain **Family:** Fumble-like
						Fold: Ribonuclease H-like motif

79	d1woqa2	Alignment	not modelled	74.7	24	**Superfamily:**Actin-like ATPase domain **Family:**ROK
80	c2f9tB_	Alignment	not modelled	73.5	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the type iii coaa from pseudomonas aeruginosa
81	d1r59o1	Alignment	not modelled	73.1	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
82	c1xupO_	Alignment	not modelled	71.7	13	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
83	c3js6A_	Alignment	not modelled	71.3	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized parm protein; **PDBTitle:** crystal structure of apo psk41 parm protein
84	c3tsuA_	Alignment	not modelled	70.6	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate
85	c3cerD_	Alignment	not modelled	70.3	14	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**possible exopolyphosphatase-like protein; **PDBTitle:** crystal structure of the exopolyphosphatase-like protein2 q8g5j2. northeast structural genomics consortium target3 blr13
86	d1zbsa1	Alignment	not modelled	69.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
87	c2i7pA_	Alignment	not modelled	69.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
88	c3smpA_	Alignment	not modelled	68.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
89	d1zc6a2	Alignment	not modelled	66.1	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
90	d1vcoa1	Alignment	not modelled	65.4	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
91	c3nvbA_	Alignment	not modelled	64.6	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
92	c3nurA_	Alignment	not modelled	61.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus
93	d2p3ra2	Alignment	not modelled	60.6	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
94	c3en9B_	Alignment	not modelled	59.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**o-sialoglycoprotein endopeptidase/protein kinase; **PDBTitle:** structure of the methanococcus jannaschii kae1-bud32 fusion2 protein
95	c1t6dB_	Alignment	not modelled	59.3	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** miras phasing of the aquifex aeolicus ppx/gppa phosphatase: crystal2 structure of the type ii variant
96	d1zxoa2	Alignment	not modelled	57.5	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
97	d1zc6a1	Alignment	not modelled	55.9	9	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
98	c3mdqA_	Alignment	not modelled	52.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolyphosphatase; **PDBTitle:** crystal structure of an exopolyphosphatase (chu_0316) from cytophaga2 hutchinsonii atcc 33406 at 1.50 a resolution
99	d1bupa2	Alignment	not modelled	51.9	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
100	d2ftsa3	Alignment	not modelled	51.5	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
101	d1hnja2	Alignment	not modelled	51.4	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
102	c2fsnB_	Alignment	not modelled	49.6	13	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**hypothetical protein ta0583; **PDBTitle:** crystal structure of ta0583, an archaeal actin homolog, complex with2 adp
103	c2p9lA_	Alignment	not modelled	44.2	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**actin-like protein 3; **PDBTitle:** crystal structure of bovine arp2/3 complex
104	c3aapA_	Alignment	not modelled	43.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleoside triphosphate diphosphohydrolase i; **PDBTitle:** crystal structure of lp1ntpdase from legionella pneumophila
						PDB header:structural protein

105	c3dwlB_	Alignment	not modelled	43.5	12	**Chain:** B: **PDB Molecule:**actin-related protein 3; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
106	c3kbqA_	Alignment	not modelled	41.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ta0487; **PDBTitle:** the crystal structure of the protein cina with unknown function from2 thermoplasma acidophilum
107	d1s1ma1	Alignment	not modelled	41.1	29	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
108	c3nvaB_	Alignment	not modelled	41.0	26	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
109	d1yzya1	Alignment	not modelled	40.1	21	**Fold:**YgbK-like **Superfamily:**YgbK-like **Family:**YgbK-like
110	d1hjra_	Alignment	not modelled	40.0	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
111	d1gpma1	Alignment	not modelled	40.0	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
112	d2csba1	Alignment	not modelled	39.8	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
113	d1y5ea1	Alignment	not modelled	39.1	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
114	c4a5bA_	Alignment	not modelled	39.0	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleoside-triphosphatase 2; **PDBTitle:** crystal structure of the c258s/c268s variant of toxoplasma gondii2 nucleoside triphosphate diphosphohydrolase 1 (ntpdase1)
115	c2zzfA_	Alignment	not modelled	36.7	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
116	d2zgya2	Alignment	not modelled	36.3	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
117	d2f7wa1	Alignment	not modelled	36.3	23	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
118	c3cjpA_	Alignment	not modelled	35.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted amidohydrolase, dihydroorotase family; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase cac3332 from2 clostridium acetobutylicum
119	d1ub7a2	Alignment	not modelled	35.5	16	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
120	d1mkza_	Alignment	not modelled	35.3	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like